

## SEQ ID NO6 7 8. txt

RESULT 2

ADF93964/c

ID ADF93964 standard; DNA; 50 BP.

XX

AC ADF93964;

XX

DT 11-MAR-2004 (first entry)

XX

DE Microorganism detection probe, SEQ ID 57.

XX

KW Probe; detection; identification; microorganism; food; drug;  
KW 16S rRNA V1 region; 16S rRNA V2 region; 16S rRNA V3 region; ss.

XX

OS Staphylococcus epidermidis.

XX

PN WO2003106676-A1.

XX

PD 24-DEC-2003.

XX

PF 16-JUN-2003; 2003WO-JP007620.

XX

PR 14-JUN-2002; 2002JP-00174564.

XX

PA (HISF) HITACHI SOFTWARE ENG CO LTD.

PA (MTS-) MITSUBISHI KAGAKU BIOTECHNICAL LAB INC.

XX

PI Hashida J, Ueno S, Muto I, Naruse K, Tamura M, Matsuda K;  
PI Shimizu M, Kobayashi I, Ishiko H;

XX

DR WPI ; 2004-071565/07.

XX

PT 20-100 base probes derived from V1, V2 or V3 regions of 16S rRNA of a  
PT microorganism for specific detection and identification of the  
PT microorganism in foods and drug compositions.

XX

PS Claim 2; SEQ ID NO 57; 150pp; Japanese.

XX

CC The present invention relates to probes (ADF93908-ADF94059) for the  
 CC specific detection and identification of harmful microorganisms in  
 CC samples of foods and drug compositions. The probe sequences are derived  
 CC from the V1, V2 and/or V3 regions of the 16S rRNA of the microorganism  
 CC or its complementary sequence. Detection and identification of the  
 CC microorganism is by amplification of the complete 16S rRNA gene using  
 CC primers ADF94060 and ADF94061, labelling the amplification product (a  
 CC fluorescence label is preferred), and hybridising to the probe or probes  
 CC of the invention. The probes may be immobilised on a DNA chip. The  
 CC microorganism is selected from Actinobacillus actinomycetemcomitans,  
 CC Acinetobacter calcoaceticus, Haemophilus influenzae, Streptophomonas  
 CC maltophilia, Proteus mirabilis, Streptococcus pneumoniae, Pseudomonas  
 CC aeruginosa, Citrobacter freundii, Veillonella parvula, Providencia  
 CC stuartii, Neisseria gonorrhoeae, Streptococcus agalactiae, Moraxella  
 CC morganii, Bacteroides fragilis, Staphylococcus hominis, Staphylococcus  
 CC warneri, Staphylococcus haemolyticus, Enterobacter cloacae, Enterobacter  
 CC aerogenes, Staphylococcus epidermidis, Streptococcus constellatus,  
 CC Serratia marcescens, Streptococcus anginosus, Escherichia coli,  
 CC Klebsiella pneumoniae, Enterococcus faecalis, Enterococcus faecium,  
 CC Streptococcus sanguis, Streptococcus mitis, Streptococcus intermedius,  
 CC Listeria monocytogenes, Clostridium perfringens, Corynebacterium  
 CC aquatum, Streptococcus oralis, Staphylococcus aureus, Neisseria  
 CC menigitidis, Campylobacter fetus, Enterococcus gallinarum, Enterococcus  
 CC casseliflavus, Aeromonas hydrophila, Salmonella paratyphi, Salmonella  
 CC typhi, Streptococcus equisimilis, Streptococcus canis, Klebsiella  
 CC oxytoca, Staphylococcus saprophyticus, Pasteurella multocida, Eikenella

SEQ ID NO: 7 8.txt  
CC corrodens, Streptococcus pyogenes, Moraxella catarrhalis, Legionella  
CC pneumoniae, Mycobacterium tuberculosis, Mycobacterium avium  
CC Mycobacterium intracelulare, Mycobacterium kansasii or Mycobacterium  
CC gordonae.  
XX  
SQ Sequence 50 BP; 10 A; 12 C; 20 G; 8 T; 0 U; 0 Other;  
Query Match 100.0% Score 15; DB 2; Length 50;  
Best Local Similarity 100.0%  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TCCTCGTCTGTTGCC 15  
Db 17 TCCTCGTCTGTTGCC 3

RESULT 3  
ADF93950/c  
ID ADF93950 standard; DNA; 50 BP.  
XX  
AC ADF93950;  
XX  
DT 11-MAR-2004 (first entry)  
XX  
DE Microorganism detection probe, SEQ ID 43.  
XX  
KW Probe; detection; identification; microorganism; food; drug;  
KW 16S rRNA V1 region; 16S rRNA V2 region; 16S rRNA V3 region; ss.  
XX  
OS Staphylococcus hominis.  
XX  
PN WO2003106676-A1.  
XX  
PD 24-DEC-2003.  
XX  
PF 16-JUN-2003; 2003WO-JP007620.  
XX  
PR 14-JUN-2002; 2002JP-00174564.  
XX  
PA (HISF) HITACHI SOFTWARE ENGINEERING CO LTD.  
PA (MTS-) MITSUBISHI KAGAKU BIOTECHNICAL LAB INC.  
XX  
PI Hashida J, Ueno S, Muto I, Naruse K, Tamura M, Matsuda K;  
PI Shimizu M, Kobayashi I, Ishiko H;  
XX  
DR WPI ; 2004-071565/07.  
XX  
PT 20-100 base probes derived from V1, V2 or V3 regions of 16S rRNA of a  
PT microorganism for specific detection and identification of the  
PT microorganism in foods and drug compositions.  
XX  
PS Claim 2; SEQ ID NO 43; 150pp; Japanese.  
XX  
CC The present invention relates to probes (ADF93908-ADF94059) for the  
CC specific detection and identification of harmful microorganisms in  
CC samples of foods and drug compositions. The probe sequences are derived  
CC from the V1, V2 and/or V3 regions of the 16S rRNA of the microorganism  
CC or its complementary sequence. Detection and identification of the  
CC microorganism is by amplification of the complete 16S rRNA gene using  
CC primers ADF94060 and ADF94061, labelling the amplification product (a  
CC fluorescence label is preferred), and hybridising to the probe or probes

SEQ ID NO: 7 8.txt  
CC of the invention. The probes may be immobilised on a DNA chip. The  
CC microorganism is selected from Actinobacteria, actinomycetomycetes,  
CC Actinobacter calcoaceticus, Haemophilus influenzae, Streptophomonas  
CC malophilia, Proteus mirabilis, Streptococcus pneumoniae, Pseudomonas  
CC aeruginosa, Citrobacter freundii, Veillonella parvula, Providencia  
CC stuartii, Neisseria gonorrhoeae, Streptococcus agalactiae, Moraxella  
CC morgani, Bacteroides fragilis, Staphylococcus hominis, Staphylococcus  
CC warneri, Staphylococcus haemolyticus, Enterobacter cloacae, Enterobacter  
CC aerogenes, Staphylococcus epidermidis, Streptococcus constellatus,  
CC Serratia marcescens, Streptococcus anginosus, Escherichia coli,  
CC Klebsiella pneumoniae, Enterococcus faecalis, Enterococcus faecium  
CC Streptococcus sanguinis, Streptococcus mitis, Streptococcus intermedius,  
CC Listeria monocytogenes, Clostridium perfringens, Corynebacterium  
CC aquatum, Streptococcus oralis, Staphylococcus aureus, Neisseria  
CC meningitidis, Campylobacter fetus, Enterococcus gallinarum, Enterococcus  
CC casseliflavus, Aeromonas hydrophila, Salmonella paratyphi, Salmonella  
CC typhi, Streptococcus equisimilis, Streptococcus canis, Klebsiella  
CC oxytoca, Staphylococcus saprophyticus, Pasteurella multocida, Escherichia  
CC corrodens, Streptococcus pyogenes, Moraxella catarrhalis, Legionella  
CC pneumophila, Mycobacterium tuberculosis, Mycobacterium avium  
CC Mycobacterium intracellulare, Mycobacterium kansasii or Mycobacterium  
CC gordonae.  
XX

SQ Sequence 50 BP; 10 A; 11 C; 20 G; 9 T; 0 U; 0 Other;

Query Match 100.0% Score 15; DB 2; Length 50;  
Best Local Similarity 100.0%  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCTCGTCTGTCGC 15  
Db 17 TCCTCGTCTGTCGC 3

SEQ ID NO: 6

SULT 2  
ADF93953/c  
ID ADF93953 standard; DNA; 50 BP.  
XX  
AC ADF93953;  
XX  
DT 11-MAR-2004 (first entry)  
XX  
DE Microorganism detection probe, SEQ ID 46.  
XX  
KW Probe; detection; identification; microorganism; food; drug;  
KW 16S rRNA V1 region; 16S rRNA V2 region; 16S rRNA V3 region; ss.  
XX  
OS Staphylococcus warneri.  
XX  
PN WO2003106676-A1.  
XX  
PD 24-DEC-2003.  
XX  
PF 16-JUN-2003; 2003WO-JP007620.  
XX  
PR 14-JUN-2002; 2002JP-00174564.  
XX  
PA (HSF) HITACHI SOFTWARE ENG CO LTD.

SEQ ID NC6 7 8.txt  
PA (M TS-) M TSUBI SHI KAGAKU BI O CLI NI CAL LAB INC.  
XX  
PI Hashida J, Ueno S, Muto I, Naruse K, Tamura M, Matsuda K;  
PI Shimizu M, Kobayashi I, Ishikawa H;  
XX  
DR WPI ; 2004-071565/07.  
XX  
PT 20-100 base probes derived from V1, V2 or V3 regions of 16S rRNA of a  
PT microorganism for specific detection and identification of the  
PT microorganism in foods and drug compositions.  
XX  
PS Claim 2; SEQ ID NO 46; 150pp; Japanese.  
XX  
CC The present invention relates to probes (ADF93908- ADF94059) for the  
CC specific detection and identification of harmful microorganisms in  
CC samples of foods and drug compositions. The probe sequences are derived  
CC from the V1, V2 and/or V3 regions of the 16S rRNA of the microorganism  
CC or its complementary sequence. Detection and identification of the  
CC microorganism is by amplification of the complete 16S rRNA gene using  
CC primers ADF94060 and ADF94061, labelling the amplification product (a  
CC fluorescence label is preferred), and hybridizing to the probe or probes  
CC of the invention. The probes may be immobilized on a DNA chip. The  
CC microorganism is selected from Actinobacillus actinomycetemcomitans,  
CC Actinobacter calcoaceticus, Haemophilus influenzae, Streptorophomonas  
CC maltophilia, Proteus mirabilis, Streptococcus pneumoniae, Pseudomonas  
CC aeruginosa, Granulicatena pharetra, Veillonella parvula, Prevotella  
CC stuartii, Neisseria gonorrhoeae, Streptococcus agalactiae, Moryanella  
CC morgani, Bacteroides fragilis, Staphylococcus hominis, Staphylococcus  
CC warneri, Staphylococcus haemolyticus, Enterobacter cloacae, Enterobacter  
CC aerogenes, Staphylococcus epidermidis, Streptococcus constellatus,  
CC Serratia marcescens, Streptococcus anginosus, Escherichia coli,  
CC Klebsiella pneumoniae, Enterococcus faecalis, Enterococcus faecium,  
CC Streptococcus sanguis, Streptococcus mitis, Streptococcus intermedius,  
CC Listeria monocytogenes, Clostridium perfringens, Corynebacterium  
CC aquatum, Streptococcus oralis, Staphylococcus aureus, Neisseria  
CC meningitidis, Campylobacter fetus, Enterococcus gallinarum, Enterococcus  
CC casseliflavus, Aeromonas hydrophila, Salmonella paratyphi, Salmonella  
CC typhi, Streptococcus equisimilis, Streptococcus canis, Klebsiella  
CC oxytoca, Staphylococcus saprophyticus, Pasteurella multocida, Eikenella  
CC corrodens, Streptococcus pyogenes, Moryanella catarrhalis, Legionella  
CC pneumophila, Mycobacterium tuberculosis, Mycobacterium avium,  
CC Mycobacterium intracellulare, Mycobacterium kansasii or Mycobacterium  
CC gordonae.  
XX  
SQ Sequence 50 BP; 11 A; 10 C; 19 G; 10 T; 0 U; 0 Other;  
Query Match 100.0% Score 16; DB 2; Length 50;  
Best Local Similarity 100.0%  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTCCTTATCTGTTGGC 16  
Db 18 CTCCTTATCTGTTGGC 3

SEQ ID NO: 7

ESULT 3  
ADF93956/c  
ID ADF93956 standard; DNA; 50 BP.  
XX  
AC ADF93956;

SEQ ID NO6 7 8.txt

XX  
DT 11-MAR-2004 (first entry)  
XX  
DE Microorganism detection probe, SEQ ID 49.  
XX  
KW Probe; detection; identification; microorganism; food; drug;  
KW 16S rRNA V1 region; 16S rRNA V2 region; 16S rRNA V3 region; ss.  
XX  
QS Staphylococcus haemolyticus.  
XX  
PN WO2003106676-A1.  
XX  
PD 24-DEC-2003.  
XX  
PF 16-JUN-2003; 2003WO-JP007620.  
XX  
PR 14-JUN-2002; 2002JP-00174564.  
XX  
PA (HISF) HI TACHI SOFTWARE ENG CO LTD.  
PA (MTS-) MITSUBISHI KAGAKU BIOTECHNICAL LAB INC.  
XX  
PI Hashida J, Ueno S, Muto I, Naruse K, Tamura M, Matsuda K;  
PI Shimadzu M, Kobayashi I, Ishikawa H;  
XX  
DR WPI ; 2004-071565/07.  
XX  
PT 20-100 base probes derived from V1, V2 or V3 regions of 16S rRNA of a  
PT microorganism for specific detection and identification of the  
PT microorganism in foods and drug compositions.  
XX  
PS Claim 2; SEQ ID NO 49; 150pp; Japanese.  
XX  
CC The present invention relates to probes (ADF93908- ADF94059) for the  
CC specific detection and identification of harmful microorganisms in  
CC samples of foods and drug compositions. The probe sequences are derived  
CC from the V1, V2 and/or V3 regions of the 16S rRNA of the microorganism  
CC or its complementary sequence. Detection and identification of the  
CC microorganism is by amplification of the complete 16S rRNA gene using  
CC primers ADF94060 and ADF94061, labelling the amplification product (a  
CC fluorescence label is preferred), and hybridising to the probe or probes  
CC of the invention. The probes may be immobilised on a DNA chip. The  
CC microorganism is selected from Actinobacillus actinomycetemcomitans,  
CC Achromobacter calcoaceticus, Haemophilus influenzae, Stenotrophomonas  
CC maltophilia, Proteus mirabilis, Streptococcus pneumoniae, Pseudomonas  
CC aeruginosa, Cytrobacter freundii, Veillonella parvula, Providencia  
CC stuartii, Neisseria gonorrhoeae, Streptococcus agalactiae, Morganella  
CC morgani, Bacteroides fragilis, Staphylococcus hominis, Staphylococcus  
CC warneri, Staphylococcus haemolyticus, Enterobacter cloacae, Enterobacter  
CC aerogenes, Staphylococcus epidermidis, Streptococcus constellatus,  
CC Serratia marcescens, Streptococcus anginosus, Escherichia coli,  
CC Klebsiella pneumoniae, Enterococcus faecalis, Enterococcus faecium,  
CC Streptococcus sanguis, Streptococcus mitis, Streptococcus intermedius,  
CC Listeria monocytogenes, Clostridium perfringens, Corynebacterium  
CC aquatum, Streptococcus oralis, Staphylococcus aureus, Neisseria  
CC meningitidis, Campylobacter fetus, Enterococcus gallinarum, Enterococcus  
CC casselilloavus, Aeromonas hydrophila, Salmonella paratyphi, Salmonella  
CC typhi, Streptococcus equisimilis, Streptococcus canis, Klebsiella  
CC oxytoca, Staphylococcus saprophyticus, Pasteurella multocida, Escherichia  
CC corrodens, Streptococcus pyogenes, Mbraekella catarrhalis, Legionella  
CC pneumophila, Mycobacterium tuberculosis, Mycobacterium avium,  
CC Mycobacterium intracellulare, Mycobacterium kansasii or Mycobacterium  
CC gordonae.

SEQ I D NO: 7 8. txt  
SQ Sequence 50 BP; 11 A; 11 C; 19 G; 9 T; 0 U; 0 Other;  
Query Match 100.0% Score 16; DB 2; Length 50;  
Best Local Similarity 100.0%  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Caps 0;  
Qy 1 CTCCTTGTCTGTTGCC 16  
Db 18 CTCCTTGTCTGTTGCC 3

SEQ I D NO: 8